Claims:

1. A process for the preparation of an L-amino acid comprising:

fermenting a suitable substrate or culture medium with a microorganism of the *Enterobacteriaceae* family, which comprises an enhanced or overexpressed *rseB* gene or *rseB* gene variant, under conditions which are suitable for the expression of the *rseB* gene or suitable for formation of an rseB gene product, and

isolating or recovering the L-amino acid.

2. The process of claim 1, wherein said microorganism is a recombinant microorganism which is generated by transformation, transduction or conjugation of a microorganism of the *Enterobacteriaceae* family with a vector, wherein the vector contains an *rseB* gene or *rseB* gene variant.

3. The process of claim 1, wherein the number of *rseB* gene copies in said microorganism is increased by at least one.

4. The process of claim 1, wherein the number of *rseB* gene copies in said microorganism is increased by at least one and said increase is achieved by integration of the *rseB* gene into the chromosome of the microorganism.

5. The process of claim 1, wherein the number of *rseB* gene copies in said microorganism is increased by at least one and said increase is achieved by incorporation of a vector which replicates extrachromosomally into said microorganism.

6. The process of claim 1, wherein over-expression of the *rseB* gene or *rseB* gene variant is achieved by:

a) mutation of the promoter and regulation region or the ribosome-binding site upstream of the *rseB* gene, or

b) incorporation of an expression cassette upstream of the *rseB* gene or *rseB* gene variant.

7. The process of claim 1, characterized in that an *rseB* gene or *rseB* gene variant which is under the control of a promoter is used.

8. The process of claim 1, wherein said microorganism has at least one additional metabolite or antimetabolite resistance mutation.

9. The process of claim 1, wherein the activity or concentration of the *rseB* gene product or *rseB* gene variant product is increased by at least 10%, based on the activity or concentration of the protein in the recipient strain, by the over-expression of the rseB gene.

10. The process of claim 1, wherein said microorganism is selected from the group consisting of the genera *Escherichia*, *Erwinia*, *Providencia* and *Serratia*.

11. The process of claim 1, wherein said microorganism further comprises one or more gene(s) in which the biosynthesis pathway of the desired L-amino acid is additionally enhanced or over-expressed.

12. The process of claim 1, wherein said microorganism further comprises one or more gene(s) selected from the group consisting of:

the *thrABC* operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase,

the *pyc* gene which codes for pyruvate carboxylase,

the *pps* gene which codes for phosphoenol pyruvate synthase,

the *ppc* gene which codes for phosphoenol pyruvate carboxylase,

the *pntA* and *pntB* genes which code for transhydrogenase,

the *rhtB* gene which imparts homoserine resistance,

the *mqo* gene which codes for malate:quinone oxidoreductase,

the *rhtC* gene which imparts threonine resistance,

the *thrE* gene which codes for the threonine export protein,

the *gdhA* gene which codes for glutamate dehydrogenase,

the *hns* gene which codes for the DNA-binding protein HLP-II,

the *pgm* gene which codes for phosphoglucomutase,

the *fba* gene which codes for fructose biphosphate aldolase,

the *ptsH* gene which codes for the phosphohistidine protein hexose phosphotransferase,

the *ptsI* gene which codes for enzyme I of the phosphotransferase system,

the *crr* gene which codes for the glucose-specific IIA component,

the *ptsG* gene which codes for the glucose-specific IIBC component,

the *lrp* gene which codes for the regulator of the leucine regulon,

the *csrA* gene which codes for the global regulator Csr,

the *fadR* gene which codes for the regulator of the fad regulon,

the *iclR* gene which codes for the regulator of central intermediate metabolism,

the *mopB* gene which codes for the 10 Kd chaperone,

the *ahpC* gene which codes for the small sub-unit of alkyl hydroperoxide reductase,

the *ahpF* gene which codes for the large sub-unit of alkyl hydroperoxide reductase,

the *cysK* gene which codes for cysteine synthase A,

the *cysB* gene which codes for the regulator of the cys regulon,

the *cysJ* gene which codes for the flavoprotein of NADPH sulfite reductase,

the *cysI* gene which codes for the haemoprotein of NADPH sulfite reductase,

the *cysH* gene which codes for adenylyl sulfate reductase,

the *phoB* gene which codes for the positive regulator PhoB of the pho regulon,

the *phoR* gene which codes for the sensor protein of the pho regulon,

the *phoE* gene which codes for protein E of the outer cell membrane,

the *pykF* gene which codes for fructose-stimulated pyruvate kinase I,

the *pfkB* gene which codes for 6-phosphofructokinase II,

the *malE* gene which codes for the periplasmic binding protein of maltose transport,

the *sodA* gene which codes for superoxide dismutase,

the *rseA* gene which codes for a membrane protein with anti-sigmaE activity,

the *rseC* gene which codes for a global regulator of the sigmaE factor

the *sucA* gene which codes for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase,

the *sucB* gene which codes for the dihydrolipoyltranssuccinase E2 sub-unit of 2-ketoglutarate dehydrogenase,

the *sucC* gene which codes for the β-sub-unit of succinyl-CoA synthetase,

the *sucD* gene which codes for the α-sub-unit of succinyl-CoA synthetase,

the *adk* gene which codes for adenylate kinase,

the *hdeA* gene which codes for a periplasmic protein with a chaperonin-like function,

the *hdeB* gene which codes for a periplasmic protein with a chaperonin-like function,

the *icd* gene which codes for isocitrate dehydrogenase,

the *mglB* gene which codes for the periplasmic, galactose-binding transport protein,

the *lpd* gene which codes for dihydrolipoamide dehydrogenase,

the *aceE* gene which codes for the E1 component of the pyruvate dehydrogenase complex,

the *aceF* gene which codes for the E2 component of the pyruvate dehydrogenase complex,

the *pepB* gene which codes for aminopeptidase B and

the *aldH* gene which codes for aldehyde dehydrogenase,

is or are enhanced or over-expressed, are fermented.

13. The process of claim 1, wherein said microorganism has at least one metabolic pathway, which reduces the formation of the desired L-amino acid, eliminated or attenuated.

14. The process of claim 1, wherein said microorganism has attenuated, reduced in expression or eliminated, one or more gene(s) selected from the group consisting of:

the *tdh* gene which codes for threonine dehydrogenase,

the *mdh* gene which codes for malate dehydrogenase,

the gene product of the open reading frame (orf) *yjfA*,

the gene product of the open reading frame (orf) *ytfP*,

the *pckA* gene which codes for phosphoenol pyruvate carboxykinase,

the *poxB* gene which codes for pyruvate oxidase,

the *aceA* gene which codes for isocitrate lyase,

the *dgsA* gene which codes for the DgsA regulator of the phosphotransferase system,

the *fruR* gene which codes for the fructose repressor,

the *rpoS* gene which codes for the sigma^{38} factor,

the *aspA* gene which codes for aspartate ammonium lyase and

the *aceB* gene which codes for malate synthase A.

15. The process of claim 1, in which

a) the desired L-amino acid is concentrated in the fermentation broth or in the cells of the microorganisms, and

b) the desired product(s) is/are isolated, the biomass and/or further constituents of the fermentation broth optionally remaining in the product in an amount of ≥ 0 to 100 %.

16. The process of claim 1, wherein said L-amino acid is selected from the group consisting of L-asparagine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

17. The process of claim 1, wherein said L-amino acid is selected from the group consisting of L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine.

18. The process according to claim 1, wherein said L-amino acid is L-threonine.

19. A recombinant microorganism of the *Enterobacteriaceae* family in which the *rseB* gene, *rseB* gene variant, or nucleotide sequences which code for the *rseB* gene product are present in over-expressed form.

20. A microorganism according to claim 19, which produces L-threonine.

A process for the fermentative preparation of L-amino acids, in particular L-threonine, in which the following steps are carried out:

a) fermentation of the microorganisms of the *Enterobacteriaceae* family which produce the desired L-amino acid and in which the *rseB* gene or nucleotide sequences which code for it are enhanced, in particular over-expressed,

b) concentration of the desired L-amino acid in the medium or in the cells of the bacteria, and

c) Isolation or recovery of the desired L-amino acid.